SEQUENCE LISTING

<110> Nielsen, Allan Kent
      Rasmussen, Michael  Dolberg

<120>  Mutated prokaryotic cells with high secretion-levels

<130>  10576.204-US

<160>  26

<170>  PatentIn version 3.3

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agcggactga caggattccc agcgctgtcg ccatatgttt cttccaagca tgcattggaa     480

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<213>  Bacillus subtilis 168

<400>  2

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            20                  25                  30

Ser Arg Gln Pro Glu Lys Ala Glu Gln Leu Arg Glu Leu Ala Ala Ala
        35                  40                  45

His Asn Val Ser Asp Ser Ile His Ile Thr Ala Leu Asp Val Thr Asp
    50                  55                  60

Glu Gln Ser Ile Val Ser Phe Gly Lys Ala Val Ser Ala Tyr Ala Pro
65                  70                  75                  80

Ile Asp Leu Leu Val Asn Asn Ala Gly Thr Ala Tyr Gly Gly Phe Ile
            85                  90                  95

Glu Asp Val Pro Met Glu His Phe Arg Gln Gln Phe Glu Thr Asn Val
            100                 105                 110

Phe Gly Val Ile His Val Thr Lys Thr Val Leu Pro Tyr Ile Arg Lys
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His Gly Gly Ala Lys Ile Ile Asn Val Ser Ser Ile Ser Gly Leu Thr
    130                 135                 140

Gly Phe Pro Ala Leu Ser Pro Tyr Val Ser Ser Lys His Ala Leu Glu
145                 150                 155                 160

Gly Phe Ser Glu Ser Leu Arg Ile Glu Leu Leu Pro Phe Gly Ile Glu
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Thr Ala Leu Ile Glu Pro Gly Ser Tyr Lys Thr Ser Ile Trp Ser Thr
            180                 185                 190

Ser Leu Ser Asn Phe Met Ser Val Pro Ala Asp Asp Ser Ala Tyr His
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Gln Tyr Tyr Lys Lys Ile Leu Ser Tyr Val Gln Lys Asn Gly Glu Glu
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Ser Gly Asp Pro Gln Glu Val Ala Asp Leu Ile Tyr Gln Leu Ala Thr
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2

Lys Gln His Ile Lys Asn Leu Arg Tyr Pro Ile Gly Lys Gly Ile Lys
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Ile Leu Lys Lys Lys Leu Phe Ser
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tacatattaa atgaaagaag acagagggtt gccgaaaagc ttagccccgg taaggaaaaa     180

ctgatcggaa accttgcggt ggacggatat cacgcttgga gtgacttata caatatggtt     240

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<213>  Bacillus subtilis 168

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            20                  25                  30


Lys Pro Gly Leu Arg Asp Val Ser Tyr Ile Leu Asn Glu Arg Arg Gln
            35                  40                  45


Arg Val Ala Glu Lys Leu Ser Pro Gly Lys Glu Lys Leu Ile Gly Asn
    50                  55                  60


Leu Ala Val Asp Gly Tyr His Ala Trp Ser Asp Leu Tyr Asn Met Val
65                  70                  75                  80


Val Gly Lys Met Thr Ile Pro Tyr Glu Glu Asn Gly Glu Asn Lys Gln
                85                  90                  95


Leu Ser Val Gly Gln Ala Glu Asn Met Met Asp His Gln Asp Arg Thr
            100                 105                 110


Val Arg Lys Thr Val Tyr Glu Arg Phe Arg Gln Ala Trp Glu Ser Lys
        115                 120                 125


Gln Asp Ile Phe Ser Ser Thr Leu Asn His Leu Ala Gly Phe Arg Leu
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4

130                        135                        140


Glu Thr Tyr Lys Ala Arg Gly Trp Glu Asn Val Leu Lys Glu Pro Leu
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Ile Thr Glu Asn Lys Lys Pro Phe Val Gln Phe Leu Asn Arg Lys Ala
              180               185               190


Ser Met Leu Gly Leu Glu Lys Leu Ser Trp Tyr Asp Val Glu Ala Pro
              195               200               205               .


Ile Gly Ser Asp Gly Lys Val Tyr Ser Tyr Asp Glu Ala Ala Asn Ile
              210               215               220


Ile Thr Ser Gln Phe Ser Thr Phe Gly Lys Lys Leu Ser Ser Phe Thr
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Glu Lys Ala Phe Arg Asp Gly Trp Ile Glu Ala Glu Asp Arg Ser Gly
                  245               250               255


Lys Arg Val Gly Gly Phe Cys Thr Ser Phe Pro Asp Ser Gly Glu Ser
                  260               265               270


Arg Ile Phe Met Thr Phe Ser Gly Ser Ala Ser Asn Val Ser Thr Leu
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Ala His Glu Leu Gly His Ala Phe His Gln Glu Ala Met Leu Asn Val
              290               295               300


Arg Pro Leu Asn Arg Ser Tyr Ala Met Asn Val Ala Glu Thr Ala Ser
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Thr Phe Ala Glu Met Ile Val Ala Asp Ala Thr Val Gln Gln Ala Glu
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Thr Arg Glu Glu Lys Leu Val Leu Leu Glu Asp Lys Val Gln Arg Ser
              340               345               350


Val Ala Phe Phe Met Asn Ile His Ala Arg Phe Leu Phe Glu Thr Arg
              355               360               365


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385                 390                 395                 400

Glu Tyr His Pro Leu Phe Trp Ala Ser Lys Leu His Phe His Ile Thr
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Arg Val Pro Phe Tyr Asn Phe Pro Tyr Thr Phe Gly Tyr Leu Phe Ser
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Leu Gly Ile Tyr Ala Leu Ala Leu Glu Glu Lys Asp Thr Phe Glu Glu
            435                 440                 445

Lys Tyr Met Ala Leu Leu Arg Asp Thr Ala Ser Met Thr Val Glu Asp
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Leu Ala Met Lys His Leu Gly Ala Asp Ile Thr Lys Arg Asp Phe Trp
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1                   5                   10                  15


Lys Gly Gly Ser Gln Ser Glu Glu Phe Lys Gly Tyr Ile Glu Lys Leu
                20                  25                  30


Ser Gln Ser Leu Arg Ala Phe Gln Asp Arg Thr Asp Ala Phe Gln Val
            35                  40                  45


Pro Glu Ser Pro Glu Glu Ala Glu Gly Leu Thr Ala Leu Leu Asp Leu
        50                  55                  60


Ile Glu Gln Thr Ser Val Lys Leu Gln Gln Ala Gly Ala Phe Val Ala
65                  70                  75                  80


Cys Leu Gln Ala Gln Asn Ile Asn Asp Gln Lys Ala Ile Glu His Gln
                85                  90                  95


Ala Ser


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7

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11

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12

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13

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21

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Leu Leu Thr Ala Leu Lys Leu Ala Ser Thr His Phe Val Ile Ala Thr
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gcg cgc cat cca gaa aaa gcg gaa gct ctg cgg aac cgt ata gcg gag     144
Ala Arg His Pro Glu Lys Ala Glu Ala Leu Arg Asn Arg Ile Ala Glu      .
            35                  40                  45


ctg tcg atc gag tca tcg att gcc gtc gct gaa ctt gat gtc aca aac     192
Leu Ser Ile Glu Ser Ser Ile Ala Val Ala Glu Leu Asp Val Thr Asn
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gaa caa tcg att tcc tca ttt tcc gaa gag ctg aag cag tac gga cag     240
Glu Gln Ser Ile Ser Ser Phe Ser Glu Glu Leu Lys Gln Tyr Gly Gln
65                  70                  75                  80


ata gac gtt ctc atc aat aat gca gga acg gca tac ggc gga ttc gct     288
Ile Asp Val Leu Ile Asn Asn Ala Gly Thr Ala Tyr Gly Gly Phe Ala
                    85                  90                  95


gaa gag ctt tct ctt ggc gac tac aga aaa cag tat gac acc aat gtt     336
Glu Glu Leu Ser Leu Gly Asp Tyr Arg Lys Gln Tyr Asp Thr Asn Val
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His Ser Gly Ala Lys Ile Ile Asn Leu Ser Ser Ile Ser Gly Arg Ile
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Ala Phe Pro Ala Phe Ser Ala Tyr Ala Ser Ser Lys His Ala Val Glu
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ggc ttt tca gaa agc ctc cgc ctc gaa ctc cgt cca ttc ggc atc aat       528
Gly Phe Ser Glu Ser Leu Arg Leu Glu Leu Arg Pro Phe Gly Ile Asn
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gtg gcc gtc gtc cag ccg gga tcg tac cag acg gcg att tgg gag aca       576
Val Ala Val Val Gln Pro Gly Ser Tyr Gln Thr Ala Ile Trp Glu Thr
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tcg ttt gcc gcc caa gtc act gca cct gat gcc gaa tca cag tac aaa       624
Ser Phe Ala Ala Gln Val Thr Ala Pro Asp Ala Glu Ser Gln Tyr Lys
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Thr Tyr Phe Glu Arg Ile Ser Ala Tyr Ile Ala Ala Ser Arg Lys His
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aaa aag cgg ctg aac agg ctg cgc tat ccg atc ggc agg ggc gtc cgt       768
Lys Lys Arg Leu Asn Arg Leu Arg Tyr Pro Ile Gly Arg Gly Val Arg
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ctc tcg atc ctt ctc cac caa atc ctg cca tgg cgg att tgg gaa cgt       816
Leu Ser Ile Leu Leu His Gln Ile Leu Pro Trp Arg Ile Trp Glu Arg
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Ala Arg His Pro Glu Lys Ala Glu Ala Leu Arg Asn Arg Ile Ala Glu
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Ile Asp Val Leu Ile Asn Asn Ala Gly Thr Ala Tyr Gly Gly Phe Ala
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Glu Glu Leu Ser Leu Gly Asp Tyr Arg Lys Gln Tyr Asp Thr Asn Val
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Phe Gly Leu Val Ala Val Thr Lys Ala Val Leu Pro Tyr Met Lys Lys
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His Ser Gly Ala Lys Ile Ile Asn Leu Ser Ser Ile Ser Gly Arg Ile
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145             150             155             160

Gly Phe Ser Glu Ser Leu Arg Leu Glu Leu Arg Pro Phe Gly Ile Asn
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Val Ala Val Val Gln Pro Gly Ser Tyr Gln Thr Ala Ile Trp Glu Thr
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Ser Phe Ala Ala Gln Val Thr Ala Pro Asp Ala Glu Ser Gln Tyr Lys
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Thr Tyr Phe Glu Arg Ile Ser Ala Tyr Ile Ala Ala Ser Arg Lys His
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Tyr Gly Asn Pro Asp Asp Val Ala Glu Leu Ile Cys Arg Leu Ala Ala
225             230             235             240

Lys Lys Arg Leu Asn Arg Leu Arg Tyr Pro Ile Gly Arg Gly Val Arg
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Ala Val Ile Lys Lys Leu Leu Lys
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27

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